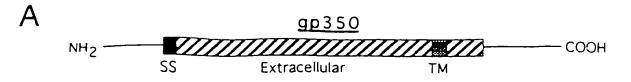
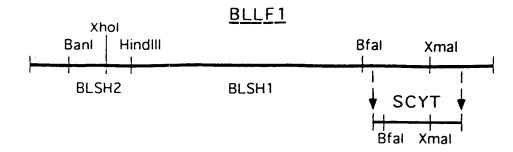
```
61 GAAGATCCTGGTTTTTTCAATGTTGAGATTCCGGAATTCCCATTTTACCCCACATGCAATGTTTGCACGGCAGATGTCAATGTAACTATCAATTTCGATGTCGGGGGCAAAAAGCATCAA GLUASPPROGLYPHEPHEASNVALGLUILEPROGLUPHEPROPHETYRPROTHRCYSASNVALCYSTHRALAASPVALASNVALTHRILEASNPHEASPVALGLYGLYLYSLYSHISGLN &C
181 CTTGATCTTGACTTTGGCCAGCTGACACCCCATACGAAGGCTGTCTACCAACCTCGAGGTGCATTTGGTGGCTCAGAAAATGCCACCAATCTCTTTCTACTGGAGGTCCCTTGGTGCAGGA
LEUASPLEUASPPHEGLYGLWLEUTHRPROHISTHRLYSALAVALTYRGLNPROARGGLYALAPHEGLYGLYSERGLUASNALATHRASNLEUPHELEULEUGLULEUGLYALAGLY
SOL GAATTGGCTCTAACTATGCGGTCTAAGAAGC*TCCAATTAACGTCACCACCGGAGAGGAGCAACAAGTAAGCCTGGAATCTGTAGATGTCTACTTTCAAGATGTGTTTGGAACCATGTGGGGLULEUALALEUTHRMETARGSERLYSLYSLEUPROILEASNVALTHRTHRGLYGLUGLUGLUGLNVALSERLEUGLUSERVALASPVALTYPHEGLNASPVALPHEGLYTHRMETTRP
341 GTCACGCTACCCTTAAGTTTGCCAACGTCAGCTCAAGACTCGAATTTCAGCGTAAAAACAGAAATGCTCGGTAATGAGATATTGAGTGTATTATGGAGGATGGCGAAATTTCACAA VALTHRLEUPROLEUSERLEUPROTHRSERALAGLNASPSERASNPHESERVALLYSTHRGLUMETLEUGLYASNGLUILEASPILEGLUCYSILEMETGLUASPGLYGLUILESERGLN 220
361 GTTCTGCCCGGAGACAAATTTAACATCACTGCACTGGATACGAGAGCCATGTTCCCAGCGGGGGAATTCTCACATCAACGAGTCCCGTGGCCACCCCAATACCTGGTACAGGGTAT
VALLEUPROGLYASPASHLYSPHEASHILETHRCYSSERGLYTYRGLUSERHISVALPROSERGLYGLYILELEUTHRSERTHRSERPROVALALATHRPROILEPROGLYTHRGLYTYR
PILIS7

781 GCATACAGCCTGCGTCTGACACCACGTCCAGTGTCACGATTTCTTGGCAATAACAGTATCCTGTACGTGTTTTACTCTGGGAATGGACCGAAGGCGAGGGGGAGATTACTGCATTCAG
ALATYRSERLEUARGLEUTHRPROARGPROVALSERARGPHELEUGLYASHASHSERILELEUTYRVALPHETYRSERGLYASHGLYPROLYSALASERGLYGLYASPTYRCYSILEGLH
TCCAACATTGTGTTCTCTGATGAGGATTCCAGGCTTCACAGGACATGCCGACAAACACCACAGACATCACATATGTGGGTGACAATGCTACCTATTCAGTGCCAATGGTCACTTCTGAGGAC
SERASNILEVALPHESERASPGLUILEPROALASERGLNASPMETPROTHRASNTHRTHRASPILETHRTYRVALGLYASPASNALATHRTYRSERVALPROMETVALTHRSERGLUASP
380
:41 GGTGCATTTGCGAGCAATCGGACATTTGACATTACTGTCTCGGGTCTTGGCACGGCCCCCAAGACACCTCATTATCACACGAACGGCTACCAATGCCACAACAACCACAAGGTTATA
GLYALAPHEALASERASNARGTHRPHEASPILETHRVALSERGLYLEUGLYTHRALAPROLYSTHRLEUILEILETHRARGTHRALATHRASNALATHRTHRTHRHISLYSVALILE
?61 TTCTCCAAGGCACCCGAGAGCACCACCACCTCCCTACCTTGAATACAACTGGATTTGCTGATCCCAATACAACGACGGTCTACCCAGCTCTACTCACGTGCCTACCAACCTCACCGCCAA PHESERLYSALAPROGLUSERTHRTHRTHRSERPROTHRLEUASNTHRTHRGLYPHEALAASPPROASNTHRTHRTHRGLYLEUPROSERSERTHRHISVALPROTHRASNLEUTHRALA
PROALASERTHROLTPROTHREAD TO THE TOTAL OF THE
321 GTGACTACCCCAACCCCAAATGCCACCAGCCCCACCTTGGGAAAAACAAGTCCTACCTCAGCAGTGACTACCCCAACCCCAAATGCCACCAGCCCCACCTTGGGAAAAACAAGCCCCACC VALTHRTHRPROTHRPROASHALATHRSERPROTHRLEUGLYLYSTHRSERPROTHR 580
TOAGCAGTGACTACCCCAAACCCCAAATGCCACCAGCCCCACCTTGGGAAAAACAAGCCCCCACCTCAGCAGTGACTACCCCAAACCCAAATGCCACCGGCCCTACTGTGGGAAAACAAGT SERALAYALTHRTHRPROTHRPROASHALATHRSERPROTHRLEUGLYLYSTHRSERPROTHRSERALAYALTHRTHRPROTHRPROASHALATHRGLYPROTHRVALGLYGLUTHRSER 620
01 AATATAACACAGGTGACACCAGCCTCTATCAGCACACATCATGTGTCCACCAGTTCGCCAGAACCCCGCCCAGGCACCACCAGCCAAGCGTCAGGCCCTGGAAACAGTTCCACACAASMILETHRGLNVALTHRPROALASEBILESERTHRISHISVALSERTHRSERSERPROGLUPROARGPROGLYTHRTHRSERGLNALASERGLYPROGLYASNSERSERTHRSERTHR
                                                                                                                                                                                                                                                          740
21 AAACCGGGGGAGGTTAATGTCACCAAAGGCACGCCCCCCAAAATGCAACGTCGCCCCAGGCCCCCAGTGGCCAAAAGACGGGGGTTCCCACGGTCACCTCAACAGGTGGAAAGGCCAAT LYSPROGLYGLUVALASHVALTHRLYSGLYTHRPROPROGLHASHALATHRSERPROGLHALAPROSERGLYGLHLYSTHRALAVALPROTHRVALTHRSERTHRGLYGLYLYSALAASH
41 TCTACCACCGGTGGAAAGCACCCACAGGACATGGAGCCCGGACAAGTACAAGGCCCACCACAGATTACGGCGGTGATTCAACTACGCCAAGACCGAGATACAATGCGACCACCTATCTA
SERTHRTHRGLYGLYLYSHISTHRTHRGLYHISGLYALAARGTHRSERTHRGLUPROTHRTHRASPTYRGLYGLYASPSERTHRTHRPROARGPROARGTYRASHALATHRTHRTYRLEU
                                                                                                                                                                                                                                                          780
                                                                                                                                                                                                                                                          820
860
                                                                                                                                                                                                                                                          900
      GATGACGCCGAGACCTATGTATAAAGTC<u>AATAAAAA</u>TTTATTAATCAGAAATTTGCACTTTCTTTGCTTCACGTCCCCGGGAGCGGGAGCGGGCACGTCGGGTGGGGTTGGGGT':TTTG %7
ASPASPALAGLUTHATYRVAL*** POLYA
     61 81 01 21 68 01 21 41
61 81 01 21
```





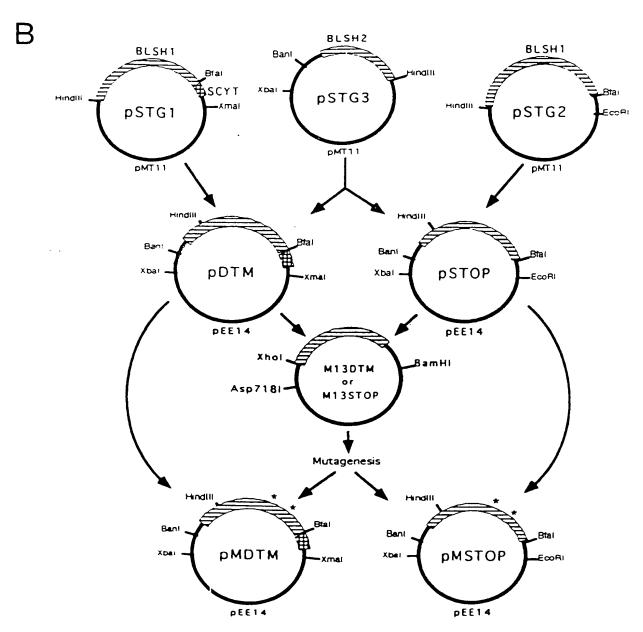


FIGURE 2

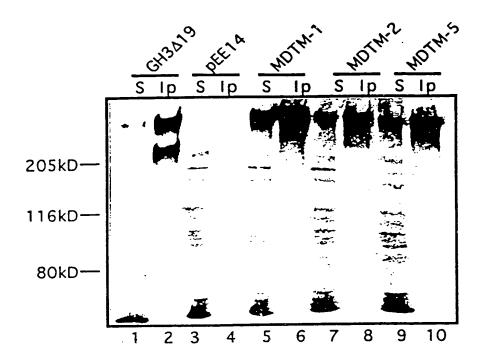


Figure 3